

ATTORNEY DOCKET NO. 14028.0295P1

SEQUENCE LISTING

<110> The Government of the United States of America, as represented by t
Secretary, Department of Health and Human Services

NEVILLE, David
WOO, Jung-Hee
LIU, Yuan-Yi

<120> METHODS FOR EXPRESSION AND PURIFICATION
OF IMMUNOTOXINS

<130> 14028.0295P1

<140> Unassigned

<141> 2004-08-02

<150> 60/491,923

<151> 2003-08-01

<160> 35

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 22

<212> PRT

<213> H. sapiens

<400> 1

Asp	Val	Thr	Leu	His	Ala	Asp	Ala	Ile	His	Arg	Gly	Gly	Gly	Gln	Ile
1				5				10						15	
Ile	Pro	Thr	Ala	Arg	Arg										
			20												

<210> 2

<211> 22

<212> PRT

<213> M. musculus

<400> 2

Asp	Val	Thr	Leu	His	Ala	Asp	Ala	Ile	His	Arg	Gly	Gly	Gly	Gln	Ile
1				5				10						15	
Ile	Pro	Thr	Ala	Arg	Arg										
			20												

<210> 3

<211> 22

<212> PRT

<213> R. norvegicus

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<400> 3

Asp	Val	Thr	Leu	His	Ala	Asp	Ala	Ile	His	Arg	Gly	Gly	Gly	Gln	Ile
1				5					10					15	
Ile	Pro	Thr	Ala	Arg	Arg										
			20												

<210> 4

<211> 22

<212> PRT

<213> C. griseus

<400> 4

Asp	Val	Thr	Leu	His	Ala	Asp	Ala	Ile	His	Arg	Gly	Gly	Gly	Gln	Ile
1				5					10					15	
Ile	Pro	Thr	Ala	Arg	Arg										
			20												

<210> 5

<211> 22

<212> PRT

<213> D. melanogaster

<400> 5

Asp	Val	Thr	Leu	His	Ala	Asp	Ala	Ile	His	Arg	Gly	Gly	Gly	Gln	Ile
1				5					10					15	
Ile	Pro	Thr	Thr	Arg	Arg										
			20												

<210> 6

<211> 22

<212> PRT

<213> C. elegans

<400> 6

Asp	Val	Thr	Leu	His	Ala	Asp	Ala	Ile	His	Arg	Gly	Gly	Gly	Gln	Ile
1				5					10					15	
Ile	Pro	Thr	Ala	Arg	Arg										
			20												

<210> 7

<211> 22

<212> PRT

<213> S. pombe

<400> 7

Asp	Val	Val	Leu	His	Ala	Asp	Ala	Ile	His	Arg	Gly	Gly	Gly	Gln	Ile
1				5					10					15	
Ile	Pro	Thr	Ala	Arg	Arg										
			20												

<210> 8

<211> 22

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<212> PRT

<213> *P. pastoris*

<400> 8

Asp	Val	Thr	Leu	His	Ala	Asp	Ala	Ile	His	Arg	Gly	Gly	Gly	Gln	Val
1				5				10						15	
Ile	Pro	Thr	Met	Lys	Arg										
			20												

<210> 9

<211> 22

<212> PRT

<213> *S. cerevisiae*

<400> 9

Asp	Val	Thr	Leu	His	Ala	Asp	Ala	Ile	His	Arg	Gly	Gly	Gly	Gln	Ile
1				5				10						15	
Ile	Pro	Thr	Met	Arg	Arg										
			20												

<210> 10

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 10

gatgttaccc	tgccacgccga	tgctatccac	cgccgcggag	gacaagtcac	tccaaccatg	60
aagaga						66

<210> 11

<211> 223

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 11

actttgaagt	tcttaatttt	gttcctcgta	gaaagaacgc	atagataatt	caaaatggca	60
aaatgggtat	gtgttttttt	atagttcatg	tgccgaacaa	ctaccgtttt	aacttcactg	120
tcgatcagat	gcgatccctt	atggacaagg	tgtccaacgt	ccgtaacatg	tcggttattg	180
cccacggtga	tcacggttaag	tccactttaa	ctgactccct	ggt		223

<210> 12

<211> 250

<212> DNA

<213> Artificial Sequence

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<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 12

acttttgaagt	tcttaattttt	gttcctcgta	gaaagaacgc	atagataatt	caaaatgggt	60
atgtgttttt	ttatagttca	tgtgccgaac	aactaccgtt	tcaagatggg	agccagccac	120
taacatctcc	tctagttaac	ttcactgtcg	atcagatgcg	atcccttatg	gacaaggtga	180
ccaacgtccg	taacatgtcg	gttattgccc	acgttgatca	cggtaagtcc	actttaactg	240
actccctggg						250

<210> 13

<211> 2601

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 13

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aacatgtcgg	ttattgccc	cgttgatcac	ggtaagtcca	ctttaactga	ctccctgggtg	120
caacgtgccg	gtattatttc	tgtgcgaag	gctggtgagg	cccgtttcac	tgatactaga	180
aaggacgagc	aagagagagg	tatcaccatc	aagtctaccg	ccatttcctt	gtactctgag	240
atgggtgacg	acgatgtcaa	ggagatcaag	cagaagactg	aaggtaacag	tttccttata	300
aacttaattg	actccccagg	tcacgttgac	ttctcttctg	aggtcactgc	tgctctgctg	360
gttactgacg	gtgctttggg	cgtcgttgac	tgtgttgaag	gtgtctgtgt	tcaaaactgag	420
accgttttgc	gtcaagcttt	gggtgaaaga	atcaagccag	ttgttgatcat	taacaagggtc	480
gaccgtgctc	ttttggagtt	gcaagttacc	aaggaggacc	tgtaccagtc	tttcgctaga	540
accgtcgagt	ccgtaaacgt	cgttatcgct	acttacactg	acaagaccat	tggtgacaac	600
caagtctacc	cagaacaggg	taccgtcgct	ttcgggttcag	gtctgcacgg	atgggctttc	660
accgttagac	agttcgccac	tagatactcc	aagaagttcg	gtgttgacag	aatcaagatg	720
atggagcgtc	tgtggggaga	ctcttacttc	aaccctaaaga	ccaagaaatg	gaccaacaag	780
gacaaggacg	ccgctggaaa	gcctttggag	cgtgccttca	acatgttcgt	tttggaccct	840
atcttccgtc	tgtttgctgc	catcatgaac	ttcaagaagg	atgaaattcc	agttctgttg	900
gagaaattgg	agatcaacct	gaagcgtgag	gagaaggagt	tgaggggtaa	ggctcttttg	960
aaggttggtc	tgagaaagtt	cttgccagct	gccgacgctt	tggtggagat	gattgttctt	1020
caoctgcat	ctccagtcac	cgtcgaagct	tacagagccg	agactttgta	cgaagggtcca	1080
tctgatgacc	aattctgcat	tggtatcaga	gagtgtgacc	ctaaggctga	gctgatgggt	1140
tacatttcca	agatgggtgcc	aacctccgac	aaaggtagat	tctacgcctt	cggtcgtggt	1200
ttctccggta	ctgttaagtc	cgttcaaaag	gtcagaatcc	aaggctcctaa	ctacgttcca	1260
ggtaagaagg	aggacttggt	catcaaggct	gttcaaaaga	ctgttttgat	gatgggaaga	1320
accgtcgagc	ctattgacga	tgtcccagct	ggtaacattc	tggttattgt	gggtatcgac	1380
cagttcttgc	tgaagtctgg	tactcttact	accaacgaag	ccgctcacia	catgaagggtg	1440
atgaaattct	ctgtctctcc	agttgtgcaa	gttgccggtg	aggtcaagaa	cgctaattgat	1500
ctgcccgaag	tggttgaggg	tctgaagcgt	ttgtccaagt	ctgacctatg	tggttttaacc	1560
tacatctccg	agtctgggtg	gcacattggt	gctgggtactg	gtgagctgca	cttggaatc	1620
tggttgcaag	atctgcaaga	cgaccacgct	gggtgtccctc	tgaagatttc	tcctccagtt	1680
gttacctacc	gtgagactgt	cactaacgaa	tcttccatga	ctgccctgtc	caagtctcag	1740
aacaagcata	acagaattta	cctgaaggct	caaccaattg	acgaggaatt	gtctttggct	1800
atcgaagaag	gtaagggttca	cccaagagac	gacttttaaag	ccagagccag	aatcatggct	1860
gatgaatacg	gttgggacgt	cactgatgcc	agaaagatct	gggtgttctcg	tccagacggt	1920

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actggtgcc  acttagttgt  tgaccagtct  aaggctgtcc  aatacttgca  cgagatcaag  1980
gactctgttg  ttgccggttt  ccaattggct  accaaggaag  gtccaatttt  gggagaaaac  2040
atgagatccg  tcagagtcaa  catcttggat  gttaccctgc  acgccgatgc  tatccacaga  2100
ggtggaggac  aagtcattcc  aaccatgaag  agagttacct  acgccgcctt  cctgttggct  2160
gagccagcta  tccaggagcc  tatcttcttg  gtggagatcc  aatgtccaga  gaatgccatt  2220
ggtggtatct  actctgtttt  gaacaagaag  agaggtcaag  ttatctctga  ggaacaaaaga  2280
ccaggtagcc  cattgttcac  tgtcaaagct  tacttgccag  ttaacgagtc  attcggtttc  2340
accggtgaac  tgagacaagc  taccgctggt  caagctttcc  cacagatggt  gttcgaccac  2400
tgggccaaac  tgaatggtaa  cccattggac  ccagcctcca  aggtcggtga  gattgttctt  2460
gctgccagaa  agagacaggg  tatgaaggag  aacgttcctg  gttatgaaga  gtactacgac  2520
aagttgtaag  cttaatgttt  cattaactta  tttgtgtcgt  tcgtatgtct  atttacgtac  2580
ttaattcagt  gtattgttgt  t  2601

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<210> 14

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 14

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Ala His Val Asp His Gly Lys Ser Thr
1             5

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<210> 15

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 15

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Asp Glu Gln Glu Arg Gly Ile Thr Ile Lys Ser Thr Ala
1             5             10

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<210> 16

<211> 896

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 16

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Ala Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val Met Glu
1             5             10             15
Asn Phe Ala Ser Tyr His Gly Thr Lys Pro Gly Tyr Val Asp Ser Ile
20             25             30

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Gln Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr Gln Gly Asn Tyr Asp
 35 40 45
 Asp Asp Trp Lys Gly Phe Tyr Ser Thr Asp Asn Lys Tyr Asp Ala Ala
 50 55 60
 Gly Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys Ala Gly Gly
 65 70 75 80
 Val Val Lys Val Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys
 85 90 95
 Val Asp Asn Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr
 100 105 110
 Glu Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg Phe
 115 120 125
 Gly Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe Ala Glu Gly
 130 135 140
 Ser Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu Gln Ala Lys Ala Leu
 145 150 155 160
 Ser Val Glu Leu Glu Ile Asn Phe Glu Thr Arg Gly Lys Arg Gly Gln
 165 170 175
 Asp Ala Met Tyr Glu Tyr Met Ala Gln Ala Cys Ala Gly Asn Arg Val
 180 185 190
 Arg Arg Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp
 195 200 205
 Val Ile Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His
 210 215 220
 Gly Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Ala Lys Thr Val Ser
 225 230 235 240
 Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu
 245 250 255
 Glu His Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly Thr Asn Pro
 260 265 270
 Val Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln
 275 280 285
 Val Ile Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr Thr Ala Ala
 290 295 300
 Leu Ser Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly
 305 310 315 320
 Ala Val His His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu
 325 330 335
 Ser Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val
 340 345 350
 Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile Ile Asn Leu
 355 360 365
 Phe Gln Val Val His Asn Ser Tyr Asn Arg Pro Ala Tyr Ser Pro Gly
 370 375 380
 His Lys Thr Gln Pro Phe Leu Pro Trp Asp Ile Gln Met Thr Gln Thr
 385 390 395 400
 Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys
 405 410 415
 Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln Gln Lys
 420 425 430
 Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His
 435 440 445
 Ser Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
 450 455 460

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Ser	Leu	Thr	Ile	Ser	Asn	Leu	Glu	Gln	Glu	Asp	Ile	Ala	Thr	Tyr	Phe
465					470					475					480
Cys	Gln	Gln	Gly	Asn	Thr	Leu	Pro	Trp	Thr	Phe	Ala	Gly	Gly	Thr	Lys
				485					490						495
Leu	Glu	Ile	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
			500					505					510		
Gly	Gly	Ser	Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Lys
		515					520					525			
Pro	Gly	Ala	Ser	Met	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe
	530					535					540				
Thr	Gly	Tyr	Thr	Met	Asn	Trp	Val	Lys	Gln	Ser	His	Gly	Lys	Asn	Leu
545					550					555					560
Glu	Trp	Met	Gly	Leu	Ile	Asn	Pro	Tyr	Lys	Gly	Val	Ser	Thr	Tyr	Asn
				565					570						575
Gln	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser
			580					585					590		
Thr	Ala	Tyr	Met	Glu	Leu	Leu	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val
		595					600					605			
Tyr	Tyr	Cys	Ala	Arg	Ser	Gly	Tyr	Tyr	Gly	Asp	Ser	Asp	Trp	Tyr	Phe
	610					615					620				
Asp	Val	Trp	Gly	Ala	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly
625					630					635					640
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Gln	Met
				645					650					655	
Thr	Gln	Thr	Thr	Ser	Ser	Leu	Ser	Ala	Ser	Leu	Gly	Asp	Arg	Val	Thr
			660					665					670		
Ile	Ser	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Arg	Asn	Tyr	Leu	Asn	Trp	Tyr
		675					680					685			
Gln	Gln	Lys	Pro	Asp	Gly	Thr	Val	Lys	Leu	Leu	Ile	Tyr	Tyr	Thr	Ser
	690					695					700				
Arg	Leu	His	Ser	Gly	Val	Pro	Ser	Lys	Phe	Ser	Gly	Ser	Gly	Ser	Gly
705					710					715					720
Thr	Asp	Tyr	Ser	Leu	Thr	Ile	Ser	Asn	Leu	Glu	Gln	Glu	Asp	Ile	Ala
				725					730					735	
Thr	Tyr	Phe	Cys	Gln	Gln	Gly	Asn	Thr	Leu	Pro	Trp	Thr	Phe	Ala	Gly
			740					745					750		
Gly	Thr	Lys	Leu	Glu	Ile	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
		755					760					765			
Ser	Gly	Gly	Gly	Gly	Ser	Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu
	770					775					780				
Leu	Val	Lys	Pro	Gly	Ala	Ser	Met	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly
785					790					795					800
Tyr	Ser	Phe	Thr	Gly	Tyr	Thr	Met	Asn	Trp	Val	Lys	Gln	Ser	His	Gly
				805					810					815	
Lys	Asn	Leu	Glu	Trp	Met	Gly	Leu	Ile	Asn	Pro	Tyr	Lys	Gly	Val	Ser
			820					825					830		
Thr	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys
		835					840						845		
Ser	Ser	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Leu	Ser	Leu	Thr	Ser	Glu	Asp
	850					855					860				
Ser	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Ser	Gly	Tyr	Tyr	Gly	Asp	Ser	Asp
865					870					875					880
Trp	Tyr	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Leu	Thr	Val	Phe	Ser
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<210> 17
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<221> misc_feature
<222> 15
<223> S = G or C

<400> 17
ggggsggggs ggggs

15

<210> 18
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<221> misc_feature
<222> 4,8,12,16
<223> s = g or c

<400> 18
ggsgggsgg gsgggs

16

<210> 19
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<221> VARIANT
<222> 2
<223> Xaa= any amino acid

<221> VARIANT
<222> 3
<223> Xaa = s or t

<400> 19
Asn Xaa Xaa
1

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<210> 20

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 20

ttggttattg accaaactaa ggctgtccaa

30

<210> 21

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 21

acctctcttc ttgtttaaga cggagtagat

30

<210> 22

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 22

cttgcttttg cggcgcgttt tttttttttt tttttttt

39

<210> 23

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 23

gataagaatg cggccgccat ttcttggtct ttgggttgaa g

41

<210> 24

<211> 42

<212> DNA

<213> Artificial Sequence

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<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 24

gataagaatg cggccgccaa cttagttgtt gaccagtcta ag

42

<210> 25

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 25

atagctagca ctttgaagtt cttaattttg ttcctc

36

<210> 26

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 26

ataagaatgc ggccgcaagt taatgaaaca ttaagcttac aac

43

<210> 27

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 27

gaatgacttg tcctccacc

19

<210> 28

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

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<400> 28
gaatgacttg tcctccgcgg 20

<210> 29
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 29
caactagcta gcgctcacia catgaaggtc atgaaattc 39

<210> 30
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 30
agaaccgtcg agcctattga cgat 24

<210> 31
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 31
ccctgcacgc cgatgctatc cacagaagag gaggacaagt cattccaacc atgaag 56

<210> 32
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 32
gccgatgcta tccacagaag a 21

<210> 33
<211> 21

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 33

gccgatgcta tccaccgccg c

21

<210> 34

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
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<400> 34

tctcttcttg ttcaaaacag agtagatacc

30

<210> 35

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<221> misc_feature

<222> 7,15

<223> n = g,a, c or t(u)

<400> 35

gtatgtncac taacntag

18